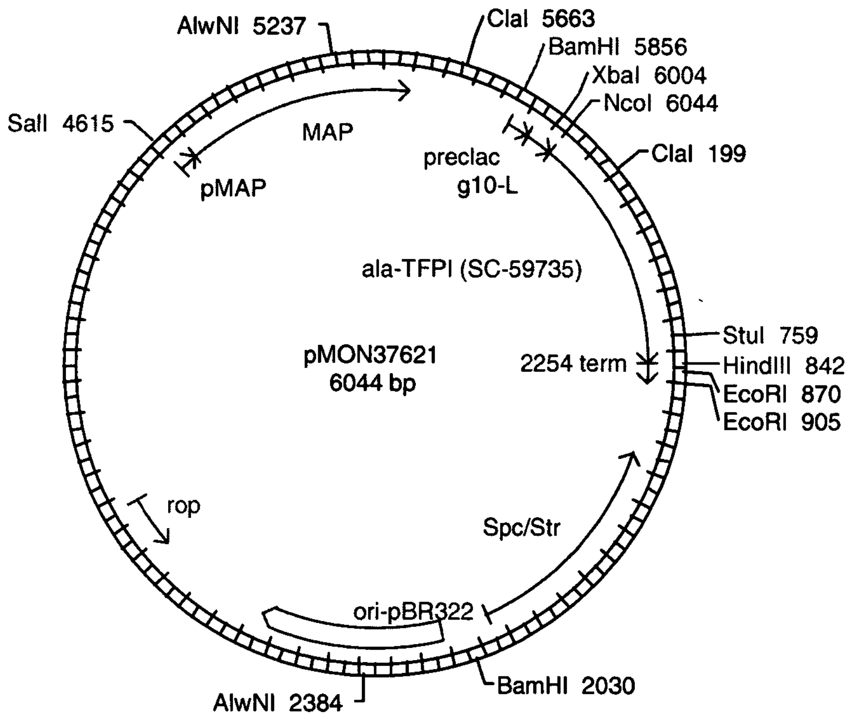
FIG. 1



AlwNI 5237
ClaI 5663
BamHI 5856
XbaI 6004
NcoI 6044
SalI 4615
ClaI 199
MAP
pMAP
preclac
g10-L
ala-TFPI (SC-59735)
pMON37621
6044 bp
2254 term
StuI 759
HindIII 842
EcoRI 870
EcoRI 905
rop
Spc/Str
ori-pBR322
AlwNI 2384
BamHI 2030

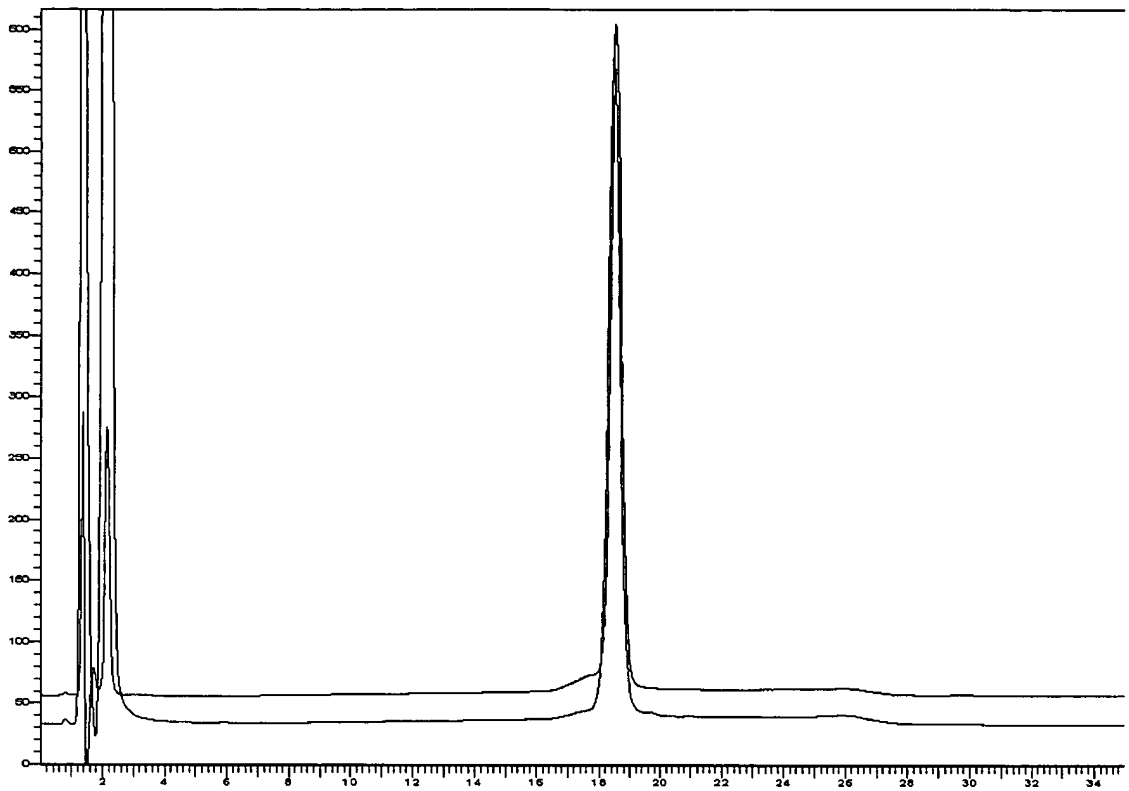
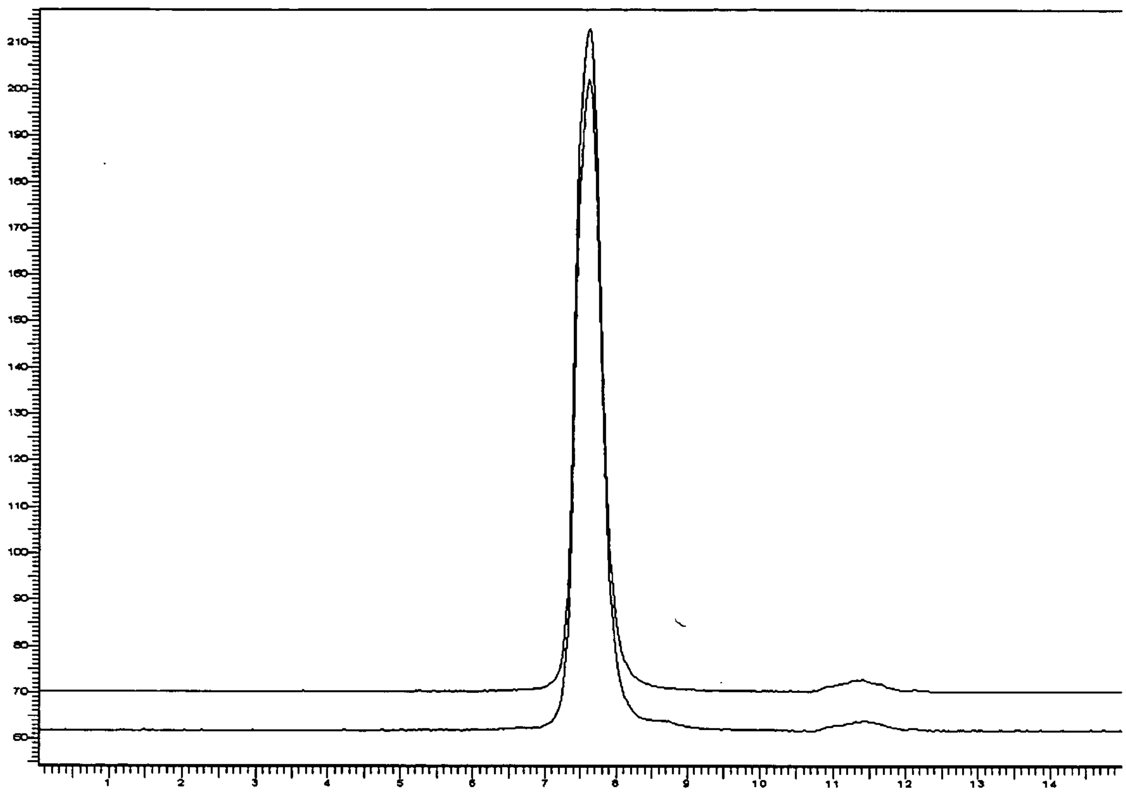


FIG. 2



210
200
190
180
170
160
150
140
130
120
110
100
90
80
70
60
1
2
3
4
5
6
7
8
9
10
11
12
13
14

FIG. 3.

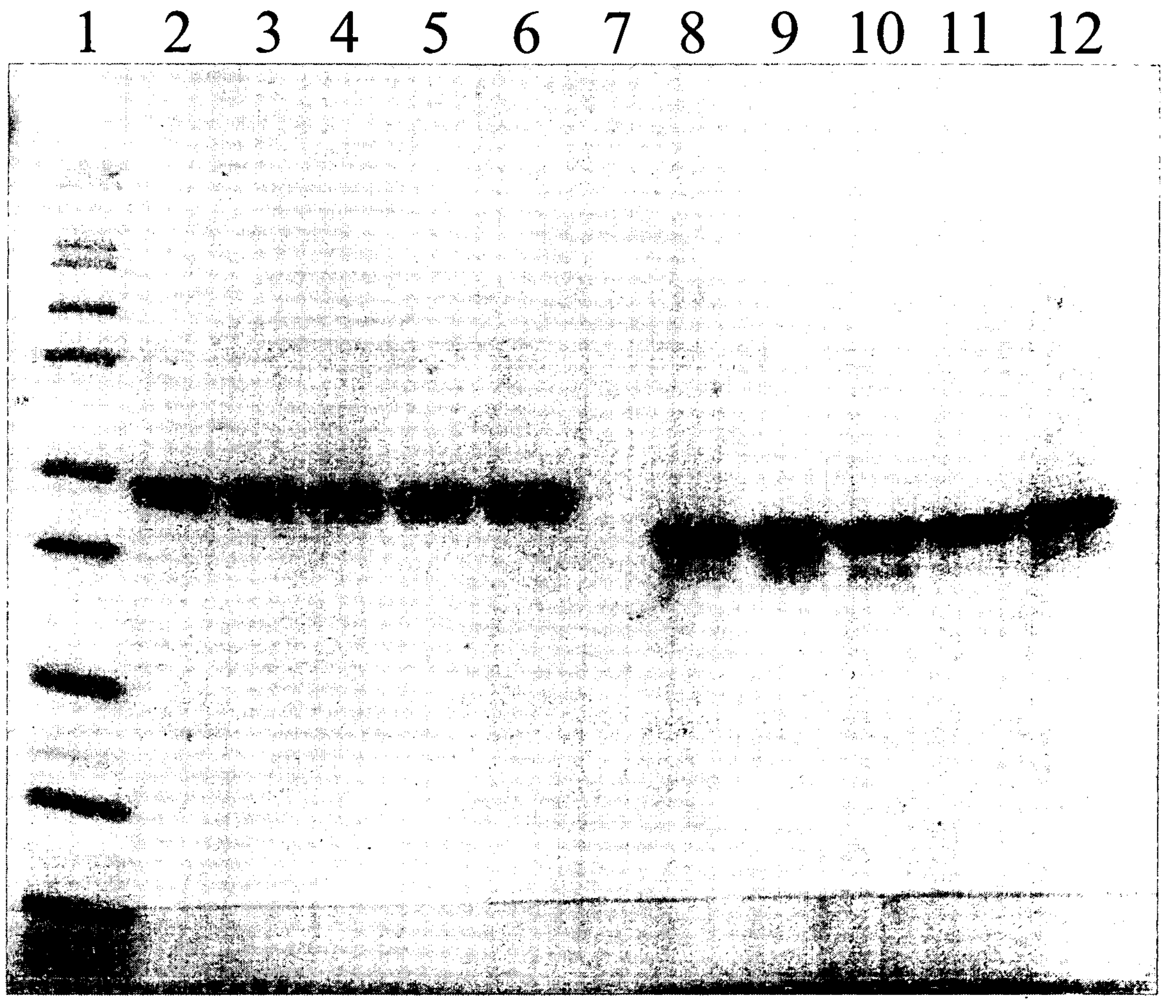


FIG. 4

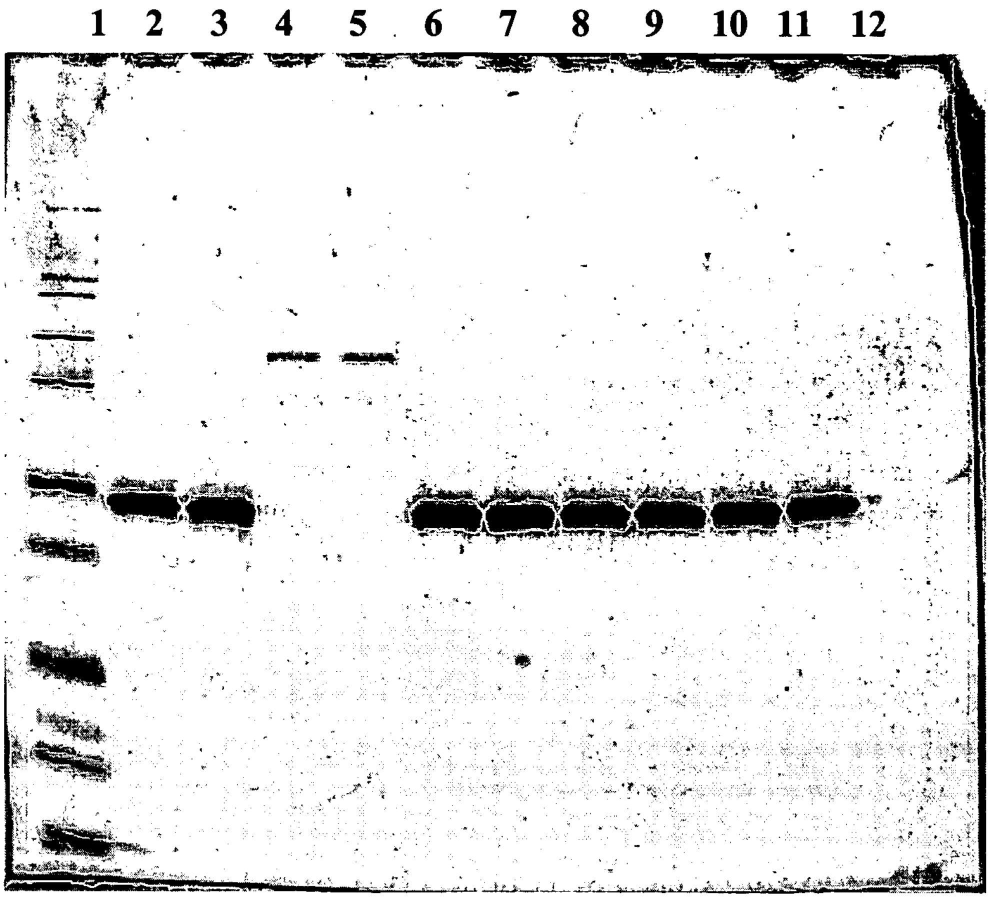


FIG. 5

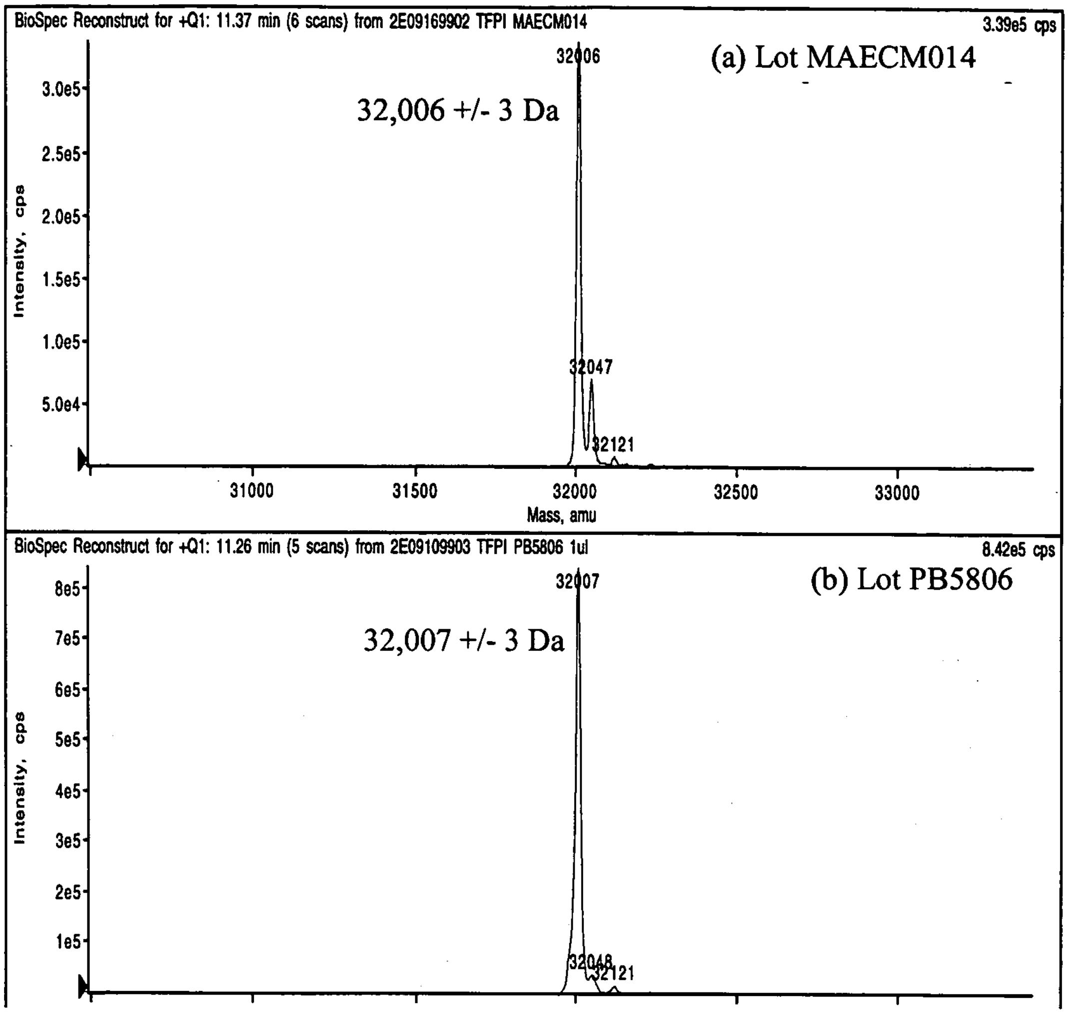

BioSpec Reconstruct for +Q1: 11.37 min (6 scans) from 2E09169902 TFPI MAECM014
3.39e5 cps
(a) Lot MAECM014
32,006 +/- 3 Da
32006
32047
32121
3.0e5
2.5e5
2.0e5
1.5e5
1.0e5
5.0e4
Intensity, cps
31000
31500
32000
32500
33000
Mass, amu
BioSpec Reconstruct for +Q1: 11.26 min (5 scans) from 2E09109903 TFPI PB5806 1ul
8.42e5 cps
(b) Lot PB5806
32,007 +/- 3 Da
32007
32048
32121
8e5
7e5
6e5
5e5
4e5
3e5
2e5
1e5
Intensity, cps

FIG. 6

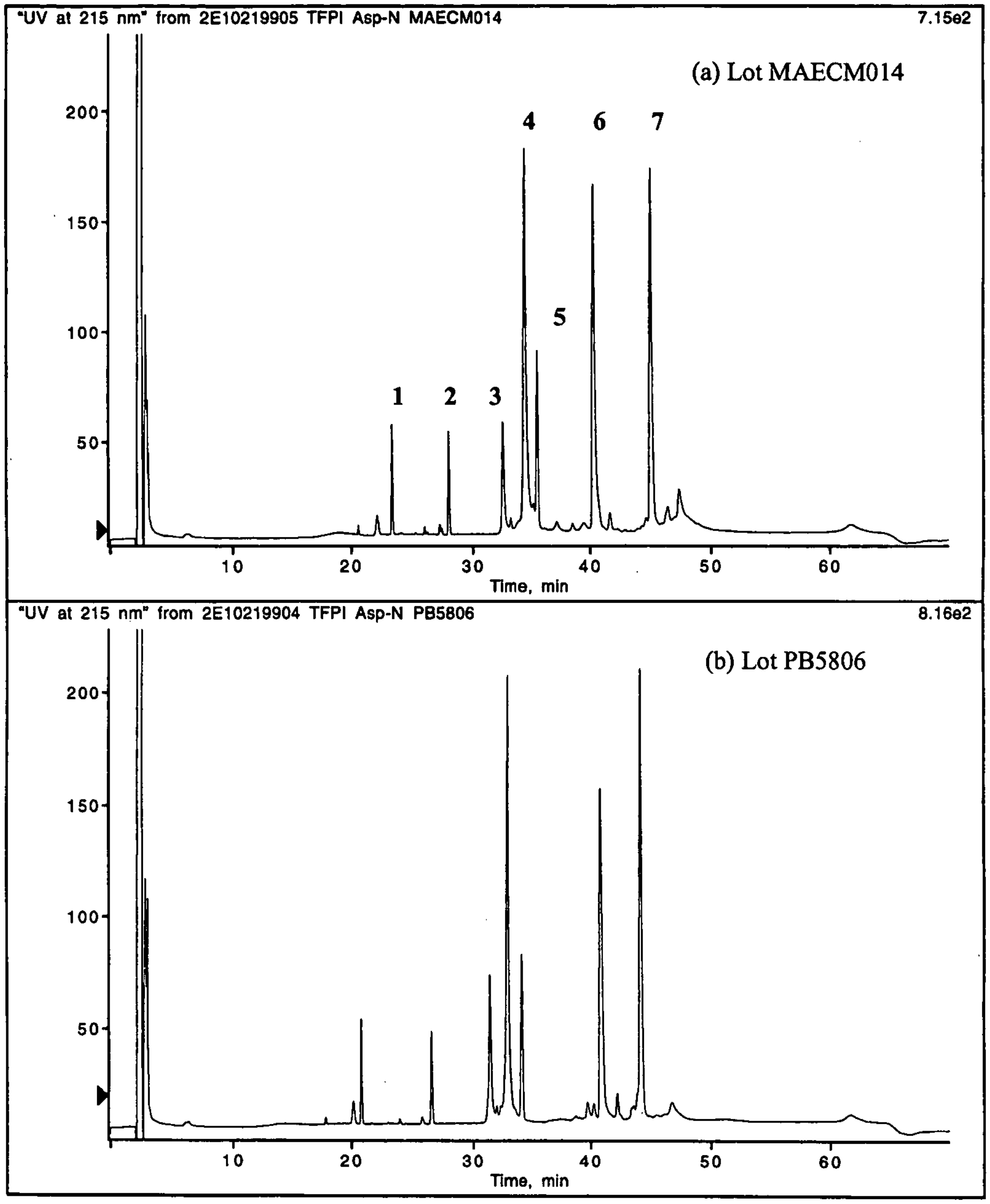
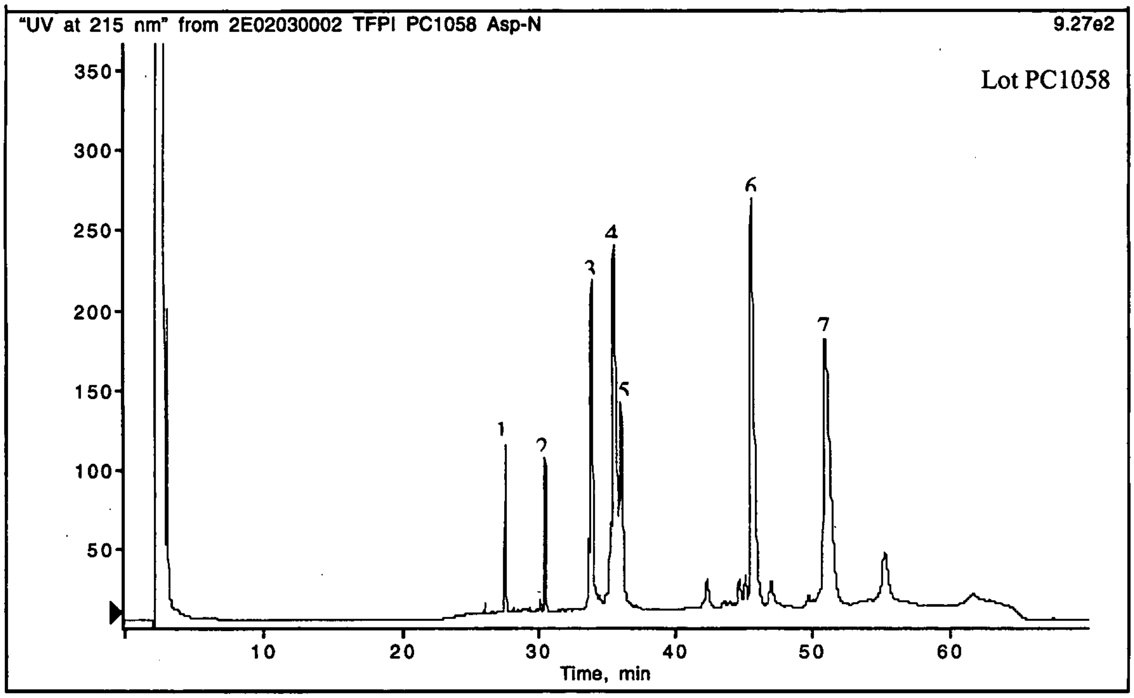

"UV at 215 nm" from 2E10219905 TFPI Asp-N MAECM014
7.15e2
(a) Lot MAECM014
1
2
3
4
5
6
7
Time, min
"UV at 215 nm" from 2E10219904 TFPI Asp-N PB5806
8.16e2
(b) Lot PB5806
Time, min

FIG. 7

FIG. 8



"UV at 215 nm" from 2E02030002 TFPI PC1058 Asp-N
9.27e2
Lot PC1058
350
300
250
200
150
100
50
10
20
30
40
50
60
Time, min
1
2
3
4
5
6
7

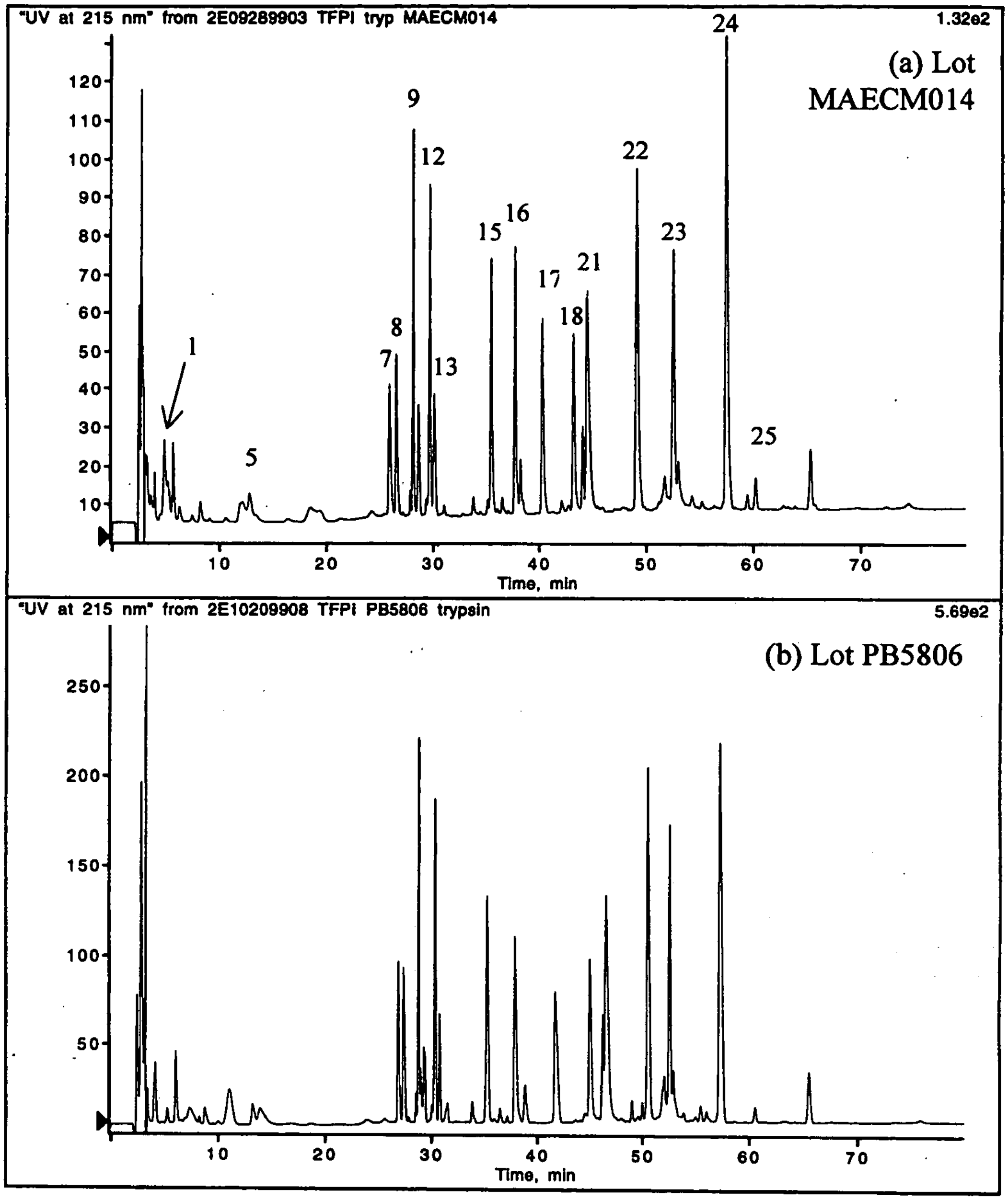
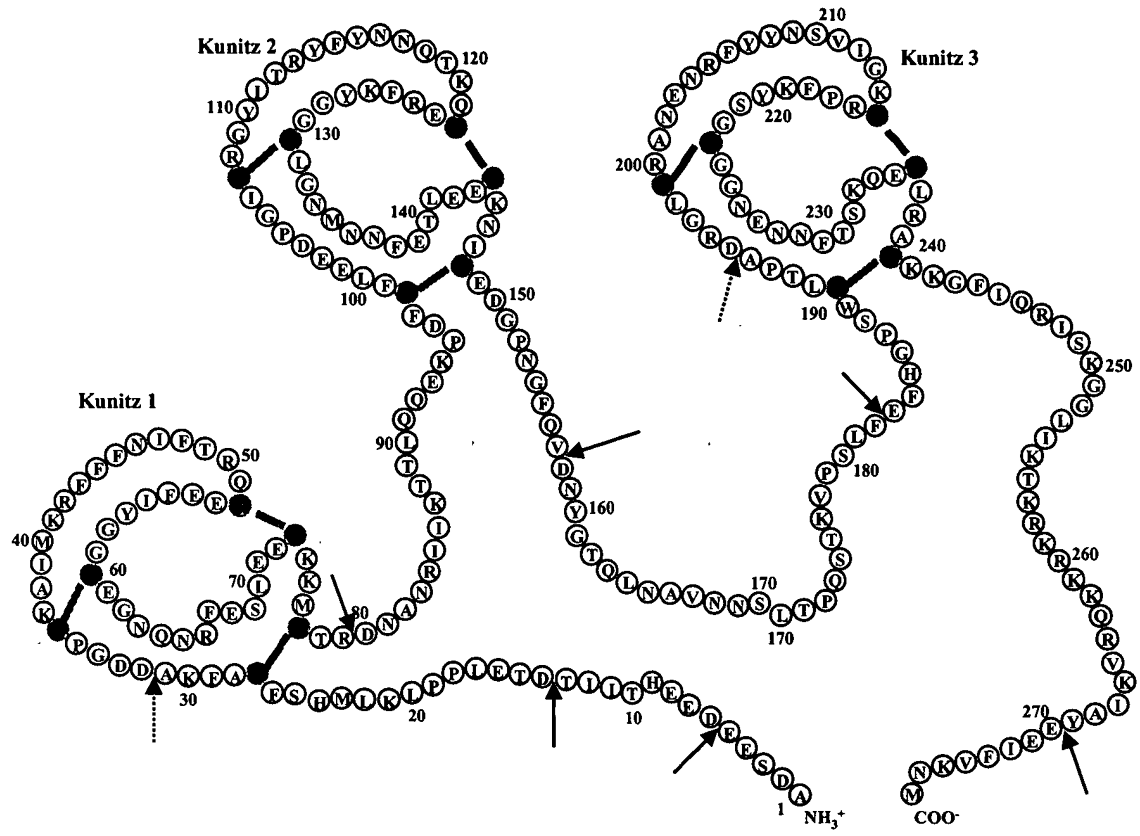

"UV at 215 nm" from 2E09289903 TFPI tryp MAECM014
1.32e2
(a) Lot MAECM014
120
110
100
90
80
70
60
50
40
30
20
10
1
5
7
8
9
12
13
15
16
17
18
21
22
23
24
25
10
20
30
40
50
60
70
Time, min
"UV at 215 nm" from 2E10209908 TFPI PB5806 trypsin
5.69e2
(b) Lot PB5806
250
200
150
100
50
10
20
30
40
50
60
70
Time, min

FIG. 9



Kunitz 1
Kunitz 2
Kunitz 3
1
10
20
30
40
50
60
70
80
90
100
110
120
130
140
150
160
170
180
190
200
210
220
230
240
250
260
270
NH_3^+
COO^-

FIG. 10

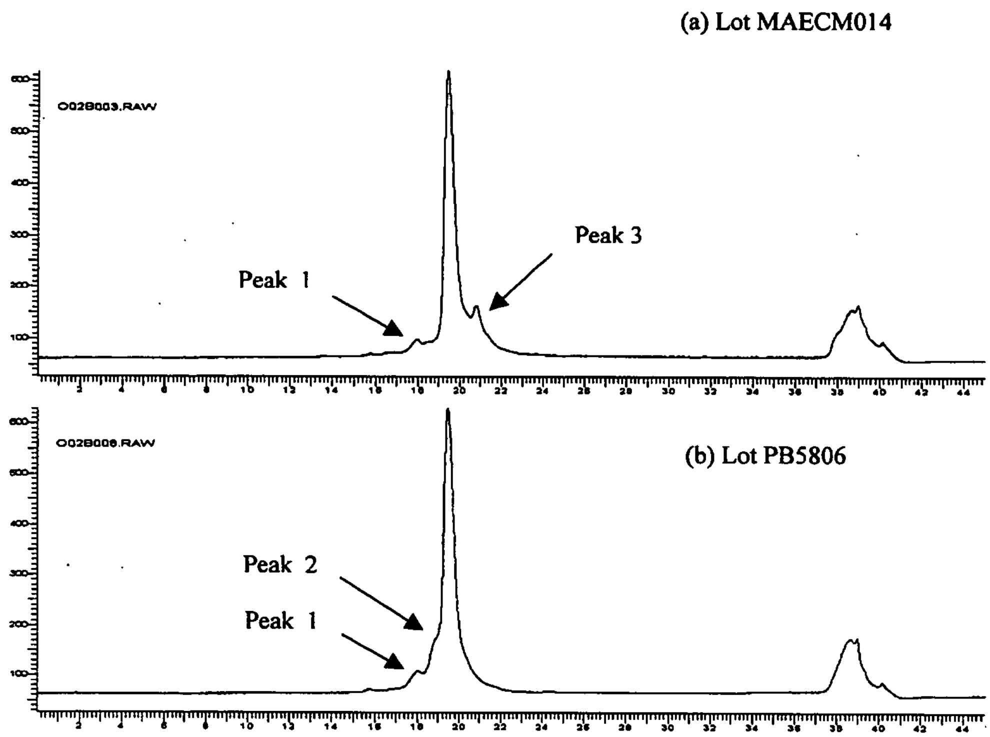

(a) Lot MAECM014
O028003.RAW
Peak 1
Peak 3
O028006.RAW
(b) Lot PB5806
Peak 2
Peak 1

FIG. 11

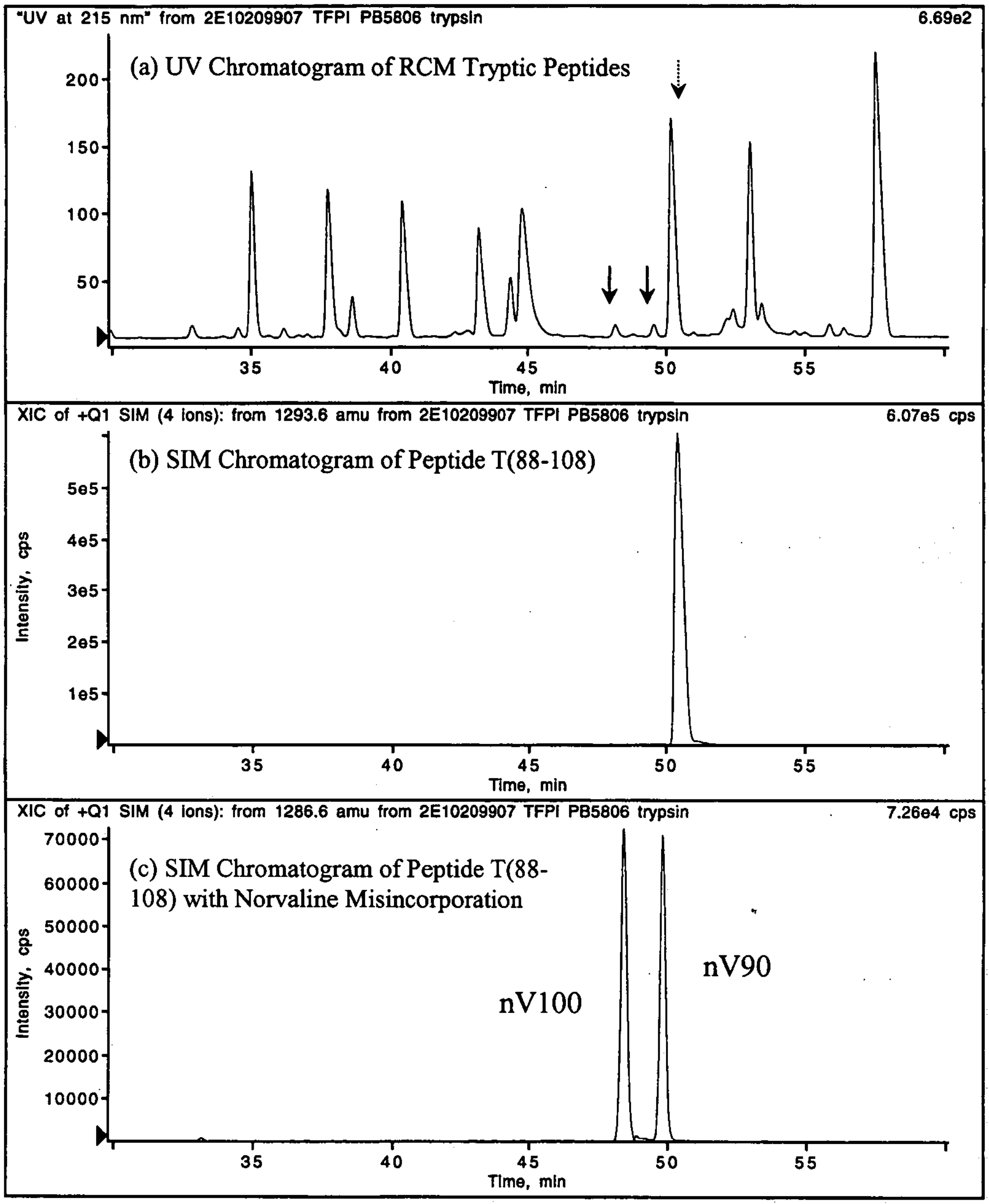

"UV at 215 nm" from 2E10209907 TFPI PB5806 trypsin
6.69e2
(a) UV Chromatogram of RCM Tryptic Peptides
200
150
100
50
35
40
45
50
55
Time, min
XIC of +Q1 SIM (4 ions): from 1293.6 amu from 2E10209907 TFPI PB5806 trypsin
6.07e5 cps
(b) SIM Chromatogram of Peptide T(88-108)
Intensity, cps
5e5
4e5
3e5
2e5
1e5
35
40
45
50
55
Time, min
XIC of +Q1 SIM (4 ions): from 1286.6 amu from 2E10209907 TFPI PB5806 trypsin
7.26e4 cps
(c) SIM Chromatogram of Peptide T(88-108) with Norvaline Misincorporation
Intensity, cps
70000
60000
50000
40000
30000
20000
10000
nV100
nV90
35
40
45
50
55
Time, min

FIG. 12

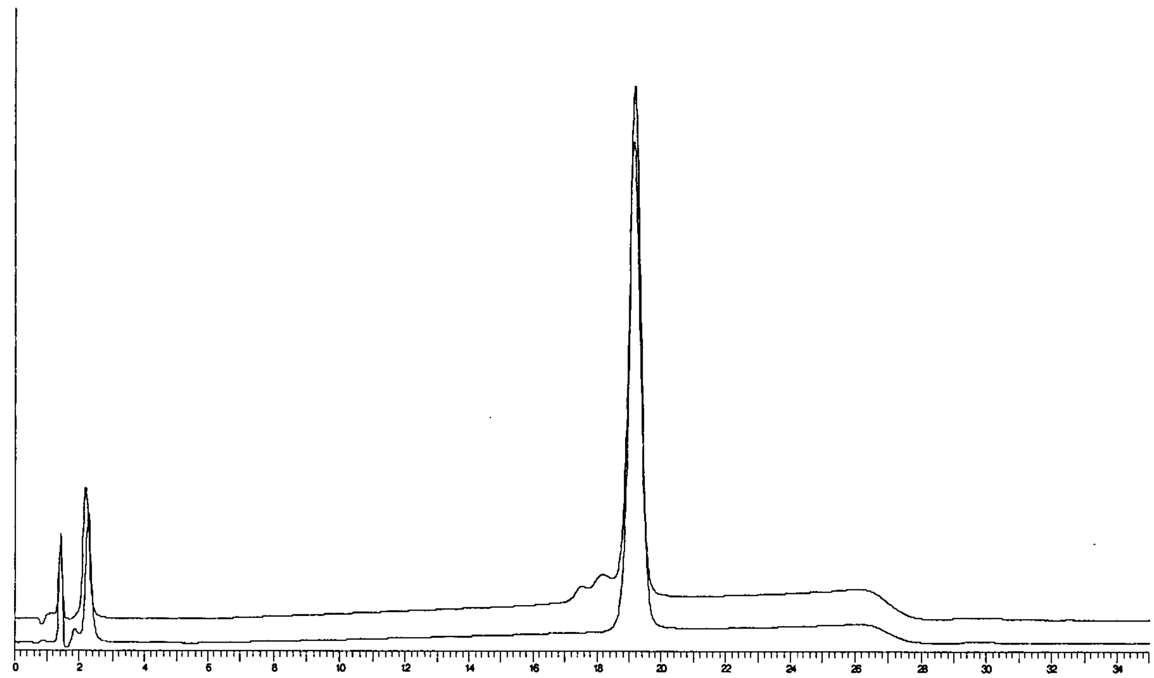
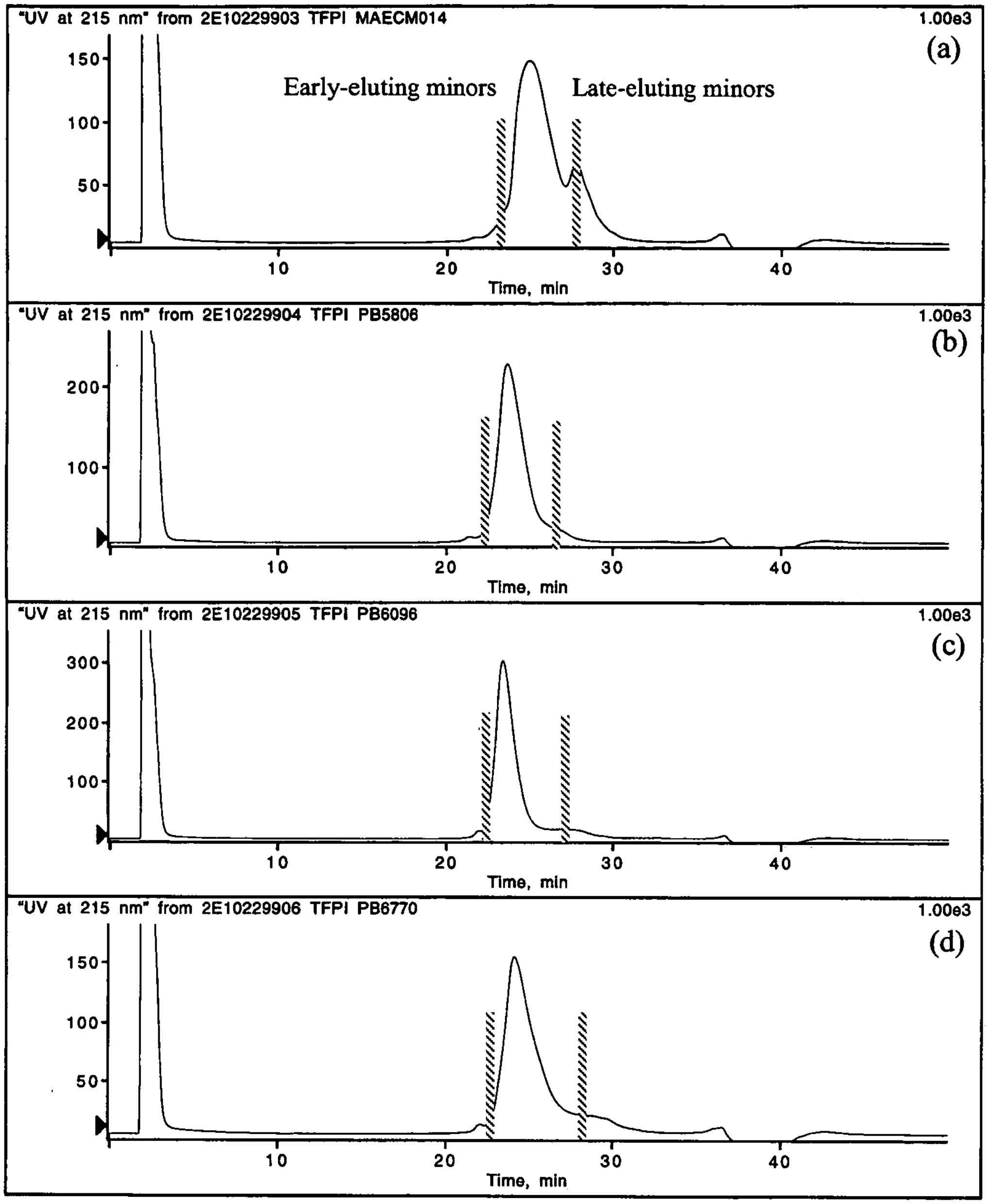


FIG. 13



"UV at 215 nm" from 2E10229903 TFPI MAECM014
1.00e3
(a)
Early-eluting minors
Late-eluting minors
150
100
50
10
20
30
40
Time, min
"UV at 215 nm" from 2E10229904 TFPI PB5806
1.00e3
(b)
200
100
10
20
30
40
Time, min
"UV at 215 nm" from 2E10229905 TFPI PB6096
1.00e3
(c)
300
200
100
10
20
30
40
Time, min
"UV at 215 nm" from 2E10229906 TFPI PB6770
1.00e3
(d)
150
100
50
10
20
30
40
Time, min

FIG. 14

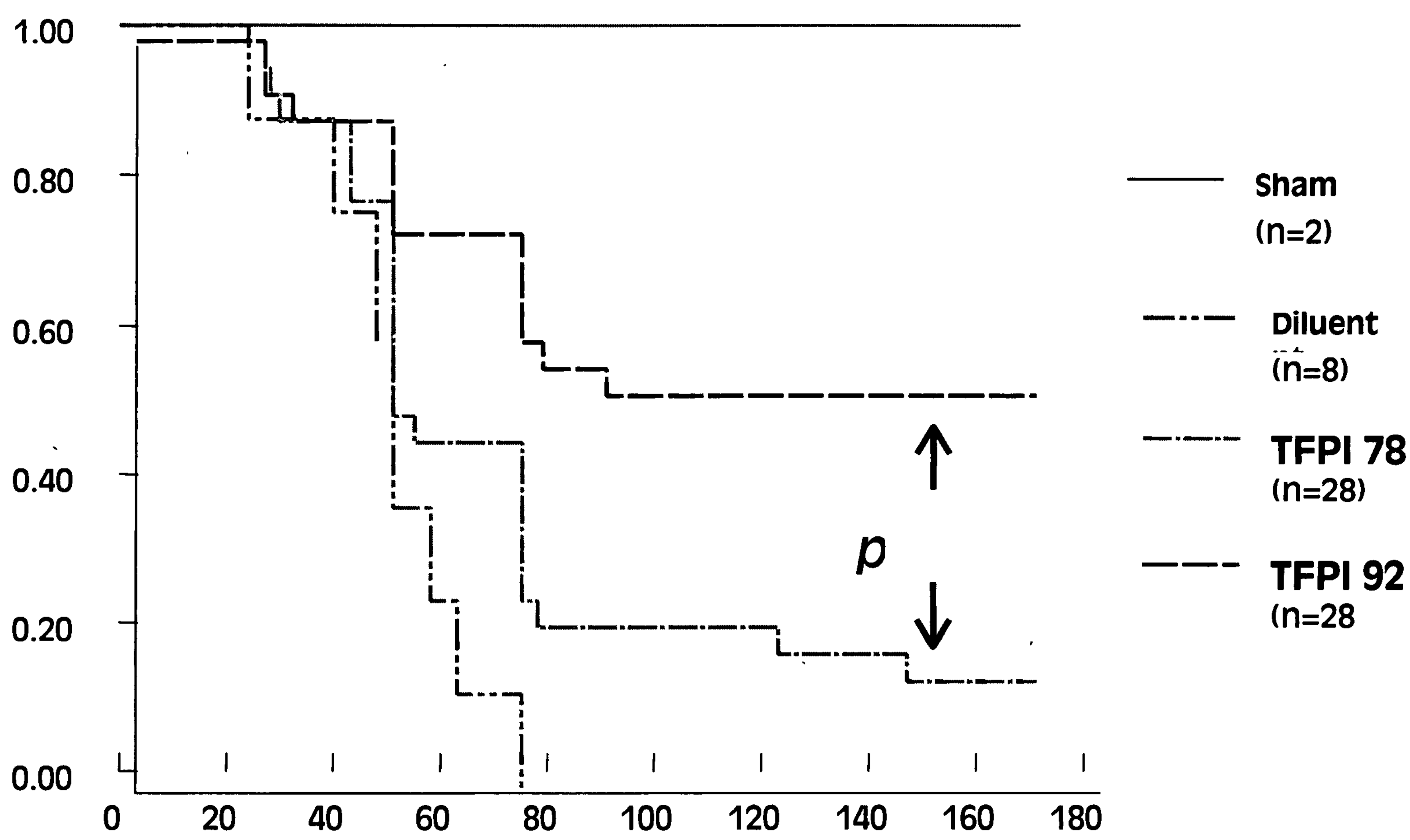
FIG. 15

```
              → tac promoter

BamHI   SacII              -35 region of         -10 region of
  |       |                   promoter           lac promoter
  GGATCCCGCGGTTCTGAAATGAGCTGTTGACAATTAATCATCGGCTCGTATAATGTGTGG
1 ---------+---------+---------+---------+---------+---------+ 60
  CCTAGGGCGCCAAGACTTTACTCGACAACTGTTAATTAGTAGCCGAGCATATTACACACC

  |→Transcription start site
  |                              BglII
  | lac operator                   |        g10-L fragment
  AATTGTGAGCGGATAACAATTTCACACAGATCTGGGCCCTTCGAAATTAATACGACTCAC
61 ---------+---------+---------+---------+---------+---------+ 120
  TTAACACTCGCCTATTGTTAAAGTGTGTCTAGACCCGGGAAGCTTTAATTATGCTGAGTG

                        XbaI                             Shine-
                          |                              Dalgarno
  TATAGGGAGACCACAACGGTTTCCCTCTAGAAATAATTTTGTTTAACTTTAAGAAGGAGA
121 ---------+---------+---------+---------+---------+---------+ 180
  ATATCCCTCTGGTGTTGCCAAAGGGAGATCTTTATTAAAACAAATTGAAATTCTTCCTCT

     NcoI
       | → Met-Ala-TFPI gene N terminus
  TATATCCATGGCTGATTCTGAAGAAGATGAAGAACATACTATTATCACTGATACTGAACT
181 ---------+---------+---------+---------+---------+---------+ 240
  ATATAGGTACCGACTAAGACTTCTTCTACTTCTTGTATGATAATAGTGACTATGACTTGA

        MetAlaAspSerGluGluAspGluGluHisThrIleIleThrAspThrGluLeu  -


                     NsiI
                      |                          T  T     A  T
  GCCACCGCTGAAACTGATGCATTCATTTTGTGCATTCAAGGCGGACGACGGCCCGTGCAA
241 ---------+---------+---------+---------+---------+---------+ 300
  CGGTGGCGACTTTGACTACGTAAGTAAAACACGTAAGTTCCGCCTGCTGCCGGGCACGTT

  ProProLeuLysLeuMetHisSerPheCysAlaPheLysAlaAspAspGlyProCysLys  -

    A        AA A  T        T  T         A
  AGCCATCATGAAGCGCTTCTTCTTCAACATCTTCACTCGTCAGTGCGAAGAATTTATATA
301 ---------+---------+---------+---------+---------+---------+ 360
  TCGGTAGTACTTCGCGAAGAAGAAGTTGTAGAAGTGAGCAGTCACGCTTCTTAAATATAT

  AlaIleMetLysArgPhePhePheAsnIlePheThrArgGlnCysGluGluPheIleTyr  -
```

```
                           ClaI
                            |
                                     AAGT  G     G     A  A
    TGGGGGATGTGAAGGAAATCAGAATCGATTTGAGTCCCTCGAAGAATGCAAGAAGATGTG
361 ---------+---------+---------+---------+---------+---------+ 420
    ACCCCCTACACTTCCTTTAGTCTTAGCTAAACTCAGGGAGCTTCTTACGTTCTTCTACAC

    GlyGlyCysGluGlyAsnGlnAsnArgPheGluSerLeuGluGluCysLysLysMetCys  -
                                                             75

    T  AA A  T  T
    CACCCGCGACAACGCAAACAGGATTATAAAGACAACATTGCAACAAGAAAAGCCAGATTT
421 ---------+---------+---------+---------+---------+---------+ 480
    GTGGGCGCTGTTGCGTTTGTCCTAATATTTCTGTTGTAACGTTGTTCTTTTCGGTCTAAA

    ThrArgAspAsnAlaAsnArgIleIleLysThrThrLeuGlnGlnGluLysProAspPhe  -

    CTGCTTTTTGGAAGAAGATCCTGGAATATGTCGAGGTTATATTACCAGGTATTTTTATAA
481 ---------+---------+---------+---------+---------+---------+ 540
    GACGAAAAACCTTCTTCTAGGACCTTATACAGCTCCAATATAATGGTCCATAAAAATATT

    CysPheLeuGluGluAspProGlyIleCysArgGlyTyrIleThrArgTyrPheTyrAsn  -

    CAATCAGACAAAACAGTGTGAACGTTTCAAGTATGGTGGATGCCTGGGCAATATGAACAA
541 ---------+---------+---------+---------+---------+---------+ 600
    GTTAGTCTGTTTTGTCACACTTGCAAAGTTCATACCACCTACGGACCCGTTATACTTGTT

    AsnGlnThrLysGlnCysGluArgPheLysTyrGlyGlyCysLeuGlyAsnMetAsnAsn  -

    TTTTGAGACACTGGAAGAATGCAAGAACATTTGTGAAGATGGTCCGAATGGTTTCCAGGT
601 ---------+---------+---------+---------+---------+---------+ 660
    AAAACTCTGTGACCTTCTTACGTTCTTGTAAACACTTCTACCAGGCTTACCAAAGGTCCA

    PheGluThrLeuGluGluCysLysAsnIleCysGluAspGlyProAsnGlyPheGlnVal  -

    GGATAATTATGGAACCCAGCTCAATGCTGTGAATAACTCCCTGACTCCGCAATCAACCAA
661 ---------+---------+---------+---------+---------+---------+ 720
    CCTATTAATACCTTGGGTCGAGTTACGACACTTATTGAGGGACTGAGGCGTTAGTTGGTT

    AspAsnTyrGlyThrGlnLeuAsnAlaValAsnAsnSerLeuThrProGlnSerThrLys  -

    GGTTCCCAGCCTTTTTGAATTTCACGGTCCCTCATGGTGTCTCACTCCAGCAGACAGAGG
721 ---------+---------+---------+---------+---------+---------+ 780
    CCAAGGGTCGGAAAAACTTAAAGTGCCAGGGAGTACCACAGAGTGAGGTCGTCTGTCTCC

    ValProSerLeuPheGluPheHisGlyProSerTrpCysLeuThrProAlaAspArgGly  -

    ATTGTGTCGTGCCAATGAGAACAGATTCTACTACAATTCAGTCATTGGGAAATGCCGCCC
781 ---------+---------+---------+---------+---------+---------+ 840
    TAACACAGCACGGTTACTCTTGTCTAAGATGATGTTAAGTCAGTAACCCTTTACGGCGGG

    LeuCysArgAlaAsnGluAsnArgPheTyrTyrAsnSerValIleGlyLysCysArgPro  -
```

```
     ATTTAAGTACAGTGGATGTGGGGGAAATGAAAACAATTTTACTTCCAAACAAGAATGTCT
 841 ---------+---------+---------+---------+---------+---------+ 900
     TAAATTCATGTCACCTACACCCCCTTTACTTTTGTTAAAATGAAGGTTTGTTCTTACAGA

     PheLysTyrSerGlyCysGlyGlyAsnGluAsnAsnPheThrSerLysGlnGluCysLeu  -

     GAGGGCATGTAAAAAAGGTTTCATCCAAAGAATATCAAAAGGAGGCCTAATTAAAACCAA
 901 ---------+---------+---------+---------+---------+---------+ 960
     CTCCCGTACATTTTTTCCAAAGTAGGTTTCTTATAGTTTTCCTCCGGATTAATTTTGGTT

     ArgAlaCysLysLysGlyPheIleGlnArgIleSerLysGlyGlyLeuIleLysThrLys  -

                                 C terminus of Ala-TFPI coding sequence
     AAGAAAAAGAAAGAAGCAGAGAGTGAAAATAGCATATGAAGAAATTTTTGTTAAAAATAT
 961 ---------+---------+---------+---------+---------+---------+ 1020
     TTCTTTTTCTTTCTTCGTCTCTCACTTTTATCGTATACTTCTTTAAAAACAATTTTTATA

     ArgLysArgLysLysGlnArgValLysIleAlaTyrGluGluIlePheValLysAsnMet  -

      Stop  HindIII
      TGA^^^AAGCTT (in pMON6655)
      | Translation Termination
      |   HindIII ClaI                       EcoRI   EcoRV P22 term delta
      |      |      |                          |       |
     GTAATAAAAGCTTATCGATGATAAGCTGTCAAACATGAGAATTCGATATCAACGCAACGA
1021 ---------+---------+---------+---------+---------+---------+ 1080
     CATTATTTTCGAATAGCTACTATTCGACAGTTTGTACTCTTAAGCTATAGTTGCGTTGCT

      EndEnd
                                  EcoRV EcoRI
                                       |   |
     CCCAGCCGAAGCTGGGTCGTTGCGTTGATATCGAATTC
1081 ---------+---------+---------+-------- 1118
     GGGTCGGCTTCGACCCAGCAACGCAACTATAGCTTAAG
```

FIG. 16



1.00
0.80
0.60
0.40
0.20
0.00
0
20
40
60
80
100
120
140
160
180
p
Sham
(n=2)
Diluent
(n=8)
TFPI 78
(n=28)
TFPI 92
(n=28